



## **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/009,817  
Source: PCT10  
Date Processed by STIC: 7/15/02

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name,  
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,  
2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,  
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

# Raw Sequence Listing Error Summary

PCT10

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 10/009, 817

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length      Sequence(s)          contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)         . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)      Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence:  
    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    (i)      SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
    (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    This sequence is intentionally skipped  
  
    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)      Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence.  
    <210> sequence id number  
    <400> sequence id number  
    000
- 9      Use of n's or Xaa's  
    (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
    In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10    Invalid <213>  
    Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>      Sequence(s)          missing the <220> "Feature" and associated numeric identifiers and responses.  
    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
    (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n      n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



PCT10

Does Not Comply  
Corrected Diskette Needed

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/009,817

DATE: 07/15/2002  
TIME: 12:39:03

Errors on pp. 4+5

Input Set : A:\Sequence Listing.txt  
Output Set: N:\CRF3\07152002\J009817.raw

```

2 <110> APPLICANT: Levy , Ilan
3     Shoseyov, Oded
4     Nussinovitch, Amos
W--> 5 <120> TITLE OF INVENTION: MODIFICATION OF POLYSACCHARIDE CONTAINING MATERIALS
W--> 6 <130> FILE REFERENCE: 00/20910
W--> 7 <140> CURRENT APPLICATION NUMBER: 60/166,389 and 60/164,140
C--> 8 <141> CURRENT FILING DATE: 2002-05-14
W--> 9 <160> NUMBER OF SEQ ID: 13
10 <170> SOFTWARE: PatentIn version 3.0
W--> 11 <210> SEQ ID NO: 1
12 <211> LENGTH: 507
13 <212> TYPE: DNA
14 <213> ORGANISM: Clostridium cellulovorans
W--> 15 <400> SEQUENCE: 1
16 ccattggcagc gacatcatca atgtcagttg aattttacaa ctctaacaaa tcagcacaaa      60
17 caaactcaat tacaccaata atcaaaatta ctaacacatc tgacagtgat ttaaatttaa      120
18 atgacgtaaa agttagatat tattacacaa gtgatggtac acaaggacaa actttctggt      180
19 gtgacctgcg tgggtgcatta ttaggaaata gctatgttga taacactagc aaagtgcacg      240
20 caaacttcgt taaagaaaaca gcaagcccaa catcaacctg tgatacatat gttgaatttg      300
21 gatttgcaag cggacgagct actcttaaaa aaggacaatt tataactatt caaggaagaa      360
22 taacaaaatc agactgggtca aactacactc aaacaaatga ctattcattt gatgcaagta      420
23 gttcaacacc agttgtaaat ccaaaaagtta caggatatat aggtggagct aaagtacttg      480
24 gtacagcacc ataggatcca gatgtac                                     507
26 <210> SEQ ID NO: 2
27 <211> LENGTH: 163
28 <212> TYPE: PRT
29 <213> ORGANISM: Clostridium cellulovorans
W--> 30 <400> SEQUENCE: 2
31 Met Ala Ala Thr Ser Ser Met Ser Val Glu Phe Tyr Asn Ser Asn Lys
32 1          5          10          15
33 Ser Ala Gln Thr Asn Ser Ile Thr Pro Ile Ile Lys Ile Thr Asn Thr
34          20          25          30
35 Ser Asp Ser Asp Leu Asn Leu Asn Asp Val Lys Val Arg Tyr Tyr Tyr
36          35          40          45
37 Thr Ser Asp Gly Thr Gln Gly Gln Thr Phe Trp Cys Asp His Ala Gly
38          50          55          60
39 Ala Leu Leu Gly Asn Ser Tyr Val Asp Asn Thr Ser Lys Val Thr Ala
40 65          70          75          80
41 Asn Phe Val Lys Glu Thr Ala Ser Pro Thr Ser Thr Tyr Asp Thr Tyr
42          85          90          95
43 Val Glu Phe Gly Phe Ala Ser Gly Arg Ala Thr Leu Lys Lys Gly Gln
44          100         105         110
45 Phe Ile Thr Ile Gln Gly Arg Ile Thr Lys Ser Asp Trp Ser Asn Tyr

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/009,817

DATE: 07/15/2002

TIME: 12:39:03

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF3\07152002\J009817.raw

```

46          115          120          125
47 Thr Gln Thr Asn Asp Tyr Ser Phe Asp Ala Ser Ser Ser Thr Pro Val
48          130          135          140
49 Val Asn Pro Lys Val Thr Gly Tyr Ile Gly Gly Ala Lys Val Leu Gly
50 145          150          155          160
51 Thr Ala Pro
54 <210> SEQ ID NO: 3
55 <211> LENGTH: 573
56 <212> TYPE: DNA
57 <213> ORGANISM: Clostridium cellulovorans
W--> 58 <400> SEQUENCE: 3
59 ccatgtcagt tgaattctac aactctaaca aatcagcaca aacaaactca attacaccaa      60
60 taatcaaaat tactaacaca tctgacagtg atttaaattt aaatgacgta aaagttagat      120
61 attattacac aagtgatggt acacaaggac aaactttctg gtgtgaccat gctggtgcat      180
62 tattaggaaa tagctatggt gataacacta gcaaagtgc agcaaacttc gttaaagaaa      240
63 cagcaagccc aacatcaacc tatgatacat atgttgaatt tggatttgca agcggacgag      300
64 ctactcttaa aaaaggacaa ttataacta ttcaaggaag aataacaaaa tcagactggt      360
65 caaactacac tcaaacaaat gactattcat ttgatgcaag tagttcaaca ccagttgtaa      420
66 atccaaaagt tacaggatat atagggtggag ctaaagtact tggtacagca ccaggtccag      480
67 atgtaccatc ttcaataatt aatcctactt ctgcaacatt tgatcccggg accatggcta      540
68 gcatgactgg tggacagcaa atgggtcggg tcc                                573
70 <210> SEQ ID NO: 4
71 <211> LENGTH: 190
72 <212> TYPE: PRT
73 <213> ORGANISM: Clostridium cellulovorans
W--> 74 <400> SEQUENCE: 4
75 Met Ser Val Glu Phe Tyr Asn Ser Asn Lys Ser Ala Gln Thr Asn Ser
76 1          5          10          15
77 Ile Thr Pro Ile Ile Lys Ile Thr Asn Thr Ser Asp Ser Asp Leu Asn
78          20          25          30
79 Leu Asn Asp Val Lys Val Arg Tyr Tyr Tyr Thr Ser Asp Gly Thr Gln
80          35          40          45
81 Gly Gln Thr Phe Trp Cys Asp His Ala Gly Ala Leu Leu Gly Asn Ser
82          50          55          60
83 Tyr Val Asp Asn Thr Ser Lys Val Thr Ala Asn Phe Val Lys Glu Thr
84 65          70          75          80
85 Ala Ser Pro Thr Ser Thr Tyr Asp Thr Tyr Val Glu Phe Gly Phe Ala
86          85          90          95
87 Ser Gly Arg Ala Thr Leu Lys Lys Gly Gln Phe Ile Thr Ile Gln Gly
88          100          105          110
89 Arg Ile Thr Lys Ser Asp Trp Ser Asn Tyr Thr Gln Thr Asn Asp Tyr
90          115          120          125
91 Ser Phe Asp Ala Ser Ser Ser Thr Pro Val Val Asn Pro Lys Val Thr
92          130          135          140
93 Gly Tyr Ile Gly Gly Ala Lys Val Leu Gly Thr Ala Pro Gly Pro Asp
94 145          150          155          160
95 Val Pro Ser Ser Ile Ile Asn Pro Thr Ser Ala Thr Phe Asp Pro Gly
96          165          170          175
97 Thr Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/009,817

DATE: 07/15/2002

TIME: 12:39:03

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF3\07152002\J009817.raw

```

98          180          185          190
100 <210> SEQ ID NO: 5
101 <211> LENGTH: 1030
102 <212> TYPE: DNA
103 <213> ORGANISM: Clostridium cellulovorans
W--> 104 <400> SEQUENCE: 5
105 ccatgtcagt tgaattctac aactctaaca aatcagcaca aacaaactca attacaccaa      60
106 taatcaaaat tactaacaca tctgacagtg atttaaattt aaatgacgta aaagttagat      120
107 attattacac aagtgatggg acacaaggac aaactttctg gtgtgaccat gctgggtgcat      180
108 tattaggaaa tagctatggt gataaacacta gcaaagtgc agcaaacttc gttaaagaaa      240
109 cagcaagccc aacatcaacc tatgatacat atgttggaatt tggatttgca agcggacgag      300
110 ctactcttaa aaaaggacaa ttataacta ttcaagggaag aataacaaaa tcagactggt      360
111 caaactacac tcaaacaaat gactattcat ttgatgcaag tagttcaaca ccagttgtaa      420
112 atccaaaagt tacaggatat ataggtggag ctaaagtact tggtagcagca ccaggtccag      480
113 atgtaccatc ttcaataatt aatcctactt ctgcaacatt tgatccccgt accatggcag      540
114 cgacatcatc aatgtcagtt gaattttaca actctaacaa atcagcaca acaaaactcaa      600
115 ttacaccaat aatcaaaaatt actaacacat ctgacagtga tttaaattta aatgacgtaa      660
116 aagttagata ttattacaca agtgatggta cacaaggaca aactttctgg tgtgaccatg      720
117 ctggtgcatt attaggaaaat agctatggtg ataacactag caaagtgcag gcaaacttcg      780
118 ttaaagaaac agcaagccca acatcaacct atgatacata tgttgaaattt ggatttgcaa      840
119 gcggaacgag tactcttaaa aaaggacaat ttataactat tcaaggaaga ataacaaaat      900
120 cagactggtc aaactacact caaacaaatg actattcatt tgatgcaagt agttcaacac      960
121 cagttgtaaa tccaaaagtt acaggatata taggtggagc taaagtactt ggtacagcac      1020
122 cataggatcc                                     1030
124 <210> SEQ ID NO: 6
125 <211> LENGTH: 340
126 <212> TYPE: PRT
127 <213> ORGANISM: Clostridium cellulovorans
W--> 128 <400> SEQUENCE: 6
129 Met Ser Val Glu Phe Tyr Asn Ser Asn Lys Ser Ala Gln Thr Asn Ser
130 1          5          10          15
131 Ile Thr Pro Ile Ile Lys Ile Thr Asn Thr Ser Asp Ser Asp Leu Asn
132          20          25          30
133 Leu Asn Asp Val Lys Val Arg Tyr Tyr Tyr Thr Ser Asp Gly Thr Gln
134          35          40          45
135 Gly Gln Thr Phe Trp Cys Asp His Ala Gly Ala Leu Leu Gly Asn Ser
136          50          55          60
137 Tyr Val Asp Asn Thr Ser Lys Val Thr Ala Asn Phe Val Lys Glu Thr
138 65          70          75          80
139 Ala Ser Pro Thr Ser Thr Tyr Asp Thr Tyr Val Glu Phe Gly Phe Ala
140          85          90          95
141 Ser Gly Arg Ala Thr Leu Lys Lys Gly Gln Phe Ile Thr Ile Gln Gly
142          100         105         110
143 Arg Ile Thr Lys Ser Asp Trp Ser Asn Tyr Thr Gln Thr Asn Asp Tyr
144          115         120         125
145 Ser Phe Asp Ala Ser Ser Ser Thr Pro Val Val Asn Pro Lys Val Thr
146          130         135         140
147 Gly Tyr Ile Gly Gly Ala Lys Val Leu Gly Thr Ala Pro Gly Pro Asp
148 145         150         155         160

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/009,817

DATE: 07/15/2002

TIME: 12:39:03

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF3\07152002\J009817.raw

```

149 Val Pro Ser Ser Ile Ile Asn Pro Thr Ser Ala Thr Phe Asp Pro Gly
150                               165                               170                               175
151 Thr Met Ala Ala Thr Ser Ser Met Ser Val Glu Phe Tyr Asn Ser Asn
152                               180                               185                               190
153 Lys Ser Ala Gln Thr Asn Ser Ile Thr Pro Ile Ile Lys Ile Thr Asn
154                               195                               200                               205
155 Thr Ser Asp Ser Asp Leu Asn Leu Asn Asp Val Lys Val Arg Tyr Tyr
156                               210                               215                               220
157 Tyr Thr Ser Asp Gly Thr Gln Gly Gln Thr Phe Trp Cys Asp His Ala
158 225                               230                               235                               240
159 Gly Ala Leu Leu Gly Asn Ser Tyr Val Asp Asn Thr Ser Lys Val Thr
160                               245                               250                               255
161 Ala Asn Phe Val Lys Glu Thr Ala Ser Pro Thr Ser Thr Tyr Asp Thr
162                               260                               265                               270
163 Tyr Val Glu Phe Gly Phe Ala Ser Gly Arg Ala Thr Leu Lys Lys Gly
164                               275                               280                               285
165 Gln Phe Ile Thr Ile Gln Gly Arg Ile Thr Lys Ser Asp Trp Ser Asn
166                               290                               295                               300
167 Tyr Thr Gln Thr Asn Asp Tyr Ser Phe Asp Ala Ser Ser Ser Thr Pro
168 305                               310                               315                               320
169 Val Val Asn Pro Lys Val Thr Gly Tyr Ile Gly Gly Ala Lys Val Leu
170                               325                               330                               335

```

171 Gly Thr Ala Pro

172 340

174 &lt;210&gt; SEQ ID NO: 7

175 &lt;211&gt; LENGTH: 1288

176 &lt;212&gt; TYPE: DNA

177 <213> ORGANISM: Recombinant nucleotide sequence

W--&gt; 178 &lt;220&gt; FEATURE:

179 &lt;221&gt; NAME/KEY: misc\_feature

180 &lt;222&gt; LOCATION: (3)..(791)

181 &lt;223&gt; OTHER INFORMATION: pRIT2T cloning vector

W--&gt; 182 &lt;220&gt; FEATURE:

183 &lt;221&gt; NAME/KEY: misc\_feature

184 &lt;222&gt; LOCATION: (795)..(1280)

185 &lt;223&gt; OTHER INFORMATION: from cbpA gene

W--&gt; 186 &lt;400&gt; SEQUENCE: 7

```

187 ccatggaaca acgcataacc ctgaaagaag cttgggatca acgcaatggt tttatccaaa      60
188 gccttaaaga tgatccaagc caaagtgcta acgttttagg tgaagctcaa aaacttaatg      120
189 actctcaagc tccaaaagct gatgcgcaac aaaataactt caacaaagat caacaaagcg      180
190 ctttctatga aatcttgaac atgcctaact taaacgaagc gcaacgtaac ggcttcattc      240
191 aaagtcttaa agacgaccca agccaaagca ctaacgtttt aggtgaagct aaaaaattaa      300
192 acgaatctca agcaccgaaa gctgataaca atttcaacaa agaacaacaa aatgctttct      360
193 atgaaatctt gaatatgcct aacttaaacg aagaacaacg caatggtttc atccaaagct      420
194 taaaagatga cccaagccaa agtgctaacc tattgtcaga agctaaaaag ttaaatgaat      480
195 ctcaagcacc gaaagcggat aacaaattca acaaagaaca acaaaatgct ttctatgaaa      540
196 ttttacatth acctaactta aacgaagaac aacgcaatgg tttcatccaa agcctaaaag      600
197 atgacccaag ccaaagcgct aaccttttag cagaagctaa aaagctaaat gatgctcaag      660
198 caccaaaagc tgacaacaaa ttcaacaaag aacaacaaaa tgctttctat gaaattttac      720

```

invalid response, see error  
summary sheet item 10

## RAW SEQUENCE LISTING

DATE: 07/15/2002

PATENT APPLICATION: US/10/009,817

TIME: 12:39:03

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF3\07152002\J009817.raw

```

199 atttacctaa cttaactgaa gaacaacgta acggcttcat ccaaagcctt aaagacgac 780
200 cggggaattc catggcagcg acatcatcaa tgtcagttga attttacaac tctaacaaat 840
201 cagcacaac aaactcaatt acaccaataa tcaaaattac taacacatct gacagtgatt 900
202 taaattttaa tgacgtaaaa gttagatatt attacacaag tgatggtaca caaggacaaa 960
203 ctttctggtg tgaccatgct ggtgcattat taggaaatag ctatggtgat aacactagca 1020
204 aagtgcagc aaacttcgtt aaagaaacag caagcccaac atcaacctat gatacatatg 1080
205 ttgaatttgg atttgcaagc ggacgagcta ctcttaaaaa aggacaattt ataactattc 1140
206 aaggaagaat aacaaaatca gactggtcaa actacactca aacaaatgac tattcatttg 1200
207 atgcaagtag ttcaacacca gttgtaaatc caaaagttac aggatatata ggtggagcta 1260
208 aagtacttgg tacagcacca taggatcc 1288

```

210 &lt;210&gt; SEQ ID NO: 8

211 &lt;211&gt; LENGTH: 426

212 &lt;212&gt; TYPE: PRT

213 &lt;213&gt; ORGANISM: recombinant protein sequence

- Same error

W--&gt; 214 &lt;220&gt; FEATURE:

215 &lt;221&gt; NAME/KEY: misc\_feature

216 &lt;222&gt; LOCATION: (1)..(263)

217 &lt;223&gt; OTHER INFORMATION: protein A from cloning vector

W--&gt; 218 &lt;220&gt; FEATURE:

219 &lt;221&gt; NAME/KEY: misc\_feature

220 &lt;222&gt; LOCATION: (265)..(426)

221 &lt;223&gt; OTHER INFORMATION: CBPA

W--&gt; 222 &lt;400&gt; SEQUENCE: 8

```

223 Met Glu Gln Arg Ile Thr Leu Lys Glu Ala Trp Asp Gln Arg Asn Gly
224 1 5 10 15
225 Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Val Leu
226 20 25 30
227 Gly Glu Ala Gln Lys Leu Asn Asp Ser Gln Ala Pro Lys Ala Asp Ala
228 35 40 45
229 Gln Gln Asn Asn Phe Asn Lys Asp Gln Gln Ser Ala Phe Tyr Glu Ile
230 50 55 60
231 Leu Asn Met Pro Asn Leu Asn Glu Ala Gln Arg Asn Gly Phe Ile Gln
232 65 70 75 80
233 Ser Leu Lys Asp Asp Pro Ser Gln Ser Thr Asn Val Leu Gly Glu Ala
234 85 90 95
235 Lys Lys Leu Asn Glu Ser Gln Ala Pro Lys Ala Asp Asn Asn Phe Asn
236 100 105 110
237 Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu Asn Met Pro Asn Leu
238 115 120 125
239 Asn Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro
240 130 135 140
241 Ser Gln Ser Ala Asn Leu Ser Glu Ala Lys Lys Leu Asn Glu Ser
242 145 150 155 160
243 Gln Ala Pro Lys Ala Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala
244 165 170 175
245 Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn
246 180 185 190
247 Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu
248 195 200 205

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## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/009,817

DATE: 07/15/2002

TIME: 12:39:04

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF3\07152002\J009817.raw

L:5 M:283 W: Missing Blank Line separator, <120> field identifier  
L:6 M:283 W: Missing Blank Line separator, <130> field identifier  
L:7 M:283 W: Missing Blank Line separator, <140> field identifier  
L:7 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:9 M:283 W: Missing Blank Line separator, <160> field identifier  
L:11 M:283 W: Missing Blank Line separator, <210> field identifier  
L:15 M:283 W: Missing Blank Line separator, <400> field identifier  
L:30 M:283 W: Missing Blank Line separator, <400> field identifier  
L:58 M:283 W: Missing Blank Line separator, <400> field identifier  
L:74 M:283 W: Missing Blank Line separator, <400> field identifier  
L:104 M:283 W: Missing Blank Line separator, <400> field identifier  
L:128 M:283 W: Missing Blank Line separator, <400> field identifier  
L:178 M:283 W: Missing Blank Line separator, <220> field identifier  
L:182 M:283 W: Missing Blank Line separator, <220> field identifier  
L:186 M:283 W: Missing Blank Line separator, <400> field identifier  
L:214 M:283 W: Missing Blank Line separator, <220> field identifier  
L:218 M:283 W: Missing Blank Line separator, <220> field identifier  
L:222 M:283 W: Missing Blank Line separator, <400> field identifier  
L:282 M:283 W: Missing Blank Line separator, <220> field identifier  
L:286 M:283 W: Missing Blank Line separator, <220> field identifier  
L:290 M:283 W: Missing Blank Line separator, <400> field identifier  
L:313 M:283 W: Missing Blank Line separator, <220> field identifier  
L:317 M:283 W: Missing Blank Line separator, <220> field identifier  
L:321 M:283 W: Missing Blank Line separator, <400> field identifier  
L:369 M:283 W: Missing Blank Line separator, <400> field identifier  
L:376 M:283 W: Missing Blank Line separator, <400> field identifier  
L:383 M:283 W: Missing Blank Line separator, <400> field identifier